RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/554,387
Source: PCT/10
Date Processed by STIC: 11/1/05

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/554,387 CRF Edit Date: 11/3/05
Edited by: [illegible]

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

✓ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

_____

___ Moved responses to same line as heading/numeric identifier, specifically:

_____

✓ Other: Sequence 8 - abgied amino acid number

_____

_____

Revised 09/09/2003

PCT

RAW SEQUENCE LISTING DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387** TIME: 12:33:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

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      3 <110> APPLICANT: Shaaltiel, Yoseph
      4       Baum, Gideon
      5       Sharon Hashmueli
      6       Ayala Lewkowicz
      7       Bartfeld, Daniel
      9 <120> TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
     11 <130> FILE REFERENCE: 30570
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/554,387
C--> 13 <141> CURRENT FILING DATE: 2005-10-25
     13 <160> NUMBER OF SEQ ID NOS: 14
     15 <170> SOFTWARE: PatentIn version 3.3
     17 <210> SEQ ID NO: 1
     18 <211> LENGTH: 22
     19 <212> TYPE: PRT
     20 <213> ORGANISM: Artificial sequence
     22 <220> FEATURE:
     23 <223> OTHER INFORMATION: ER signal peptide
     25 <400> SEQUENCE: 1
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     28 1               5                  10                  15
     31 Leu Ser Ser Ala Glu Phe
     32             20
     35 <210> SEQ ID NO: 2
     36 <211> LENGTH: 7
     37 <212> TYPE: PRT
     38 <213> ORGANISM: Artificial sequence
     40 <220> FEATURE:
     41 <223> OTHER INFORMATION: Vacuolar targeting signal from Tobacco chitinase A
     43 <400> SEQUENCE: 2
     45 Asp Leu Leu Val Asp Thr Met
     46 1               5
     49 <210> SEQ ID NO: 3
     50 <211> LENGTH: 21
     51 <212> TYPE: DNA
     52 <213> ORGANISM: Artificial sequence
     54 <220> FEATURE:
     55 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
     57 <400> SEQUENCE: 3
     58 cagaattcgc ccgcccctgc a                                          21
     61 <210> SEQ ID NO: 4
     62 <211> LENGTH: 22
     63 <212> TYPE: DNA
     64 <213> ORGANISM: Artificial sequence
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RAW SEQUENCE LISTING DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387 TIME: 12:33:35

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11032005\J554387.raw

66 <220> FEATURE:
67 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
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73 <210> SEQ ID NO: 5
74 <211> LENGTH: 19
75 <212> TYPE: DNA
79 <213> ORGANISM: Artificial sequence
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
84 <400> SEQUENCE: 5
85 ctcagaagac cagagggct 19
88 <210> SEQ ID NO: 6
89 <211> LENGTH: 17
90 <212> TYPE: DNA
91 <213> ORGANISM: Artificial sequence
93 <220> FEATURE:
94 <223> OTHER INFORMATION: Single strand DNA oligonucleotide
96 <400> SEQUENCE: 6
97 caaagcggcc atcgtgc 17
100 <210> SEQ ID NO: 7
101 <211> LENGTH: 1491
102 <212> TYPE: DNA
103 <213> ORGANISM: Homo sapiens
105 <400> SEQUENCE: 7
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108 acatactgtg actcctttga ccccccgacc tttcctgccc ttggtacctt cagccgctat 120
110 gagagtacac gcagtgggcg acggatggag ctgagtatgg ggcccatcca ggctaatcac 180
112 acgggcacag gcctgctact gaccctgcag ccagaacaga agttccagaa agtgaaggga 240
114 tttggagggg ccatgacaga tgctgctgct ctcaacatcc ttgccctgtc acccctgcc 300
116 caaaatttgc tacttaaatc gtacttctct gaagaaggaa tcggatataa catcatccgg 360
118 gtacccatgg ccagctgtga cttctccatc cgcacctaca cctatgcaga cacccctgat 420
120 gatttccagt tgcacaactt cagcctccca gaggaagata ccaagctcaa gataccctg 480
122 attcaccgag ccctgcagtt ggcccagcgt cccgtttcac tccttgccag cccctggaca 540
124 tcacccactt ggctcaagac caatggagcg gtgaatggga aggggtcact caagggacag 600
126 cccggagaca tctaccacca gacctgggcc agatactttg tgaagttcct ggatgcctat 660
128 gctgagcaca agttacagtt ctgggcagtg acagctgaaa atgagccttc tgctgggctg 720
130 ttgagtggat acccttcca gtgcctgggc ttcacccctg aacatcagcg agacttcatt 780
132 gcccgtgacc taggtcctac cctcgccaac agtactcacc acaatgtccg cctactcatg 840
134 ctggatgacc aacgcttgct gctgccccac tgggcaaagg tggtactgac agacccagaa 900
136 gcagctaaat atgttcatgg cattgctgta cattggtacc tggactttct ggctccagcc 960
138 aaagccaccc taggggagac acaccgcctg ttccccaaca ccatgctctt tgcctcagag 1020
140 gcctgtgtgg gctccaagtt ctgggagcag agtgtgcggc taggctcctg ggatcgaggg 1080
142 atgcagtaca gccacagcat catcacgaac ctcctgtacc atgtggtcgg ctggaccgac 1140
144 tggaaccttg ccctgaaccc cgaaggagga cccaattggg tgcgtaactt tgtcgacagt 1200
146 cccatcattg tagacatcac caaggacacg ttttacaaac agcccatgtt ctaccacctt 1260
148 ggccacttca gcaagttcat tcctgagggc tcccagagag tggggctggt tgccagtcag 1320
150 aagaacgacc tggacgcagt ggcactgatg catcccgatg gctctgctgt tgtggtcgtg 1380
152 ctaaaccgct cctctaagga tgtgcctctt accatcaagg atcctgctgt gggcttcctg 1440

RAW SEQUENCE LISTING DATE: 11/03/2005
PATENT APPLICATION: US/10/554,387 TIME: 12:33:35

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\11032005\J554387.raw

154 gagacaatct cacctggcta ctccattcac acctacctgt ggcatcgcca g 1491
157 <210> SEQ ID NO: 8
158 <211> LENGTH: 335
159 <212> TYPE: PRT
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 8
164 Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys
165 1 5 10 15
168 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
169 20 25 30
172 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
173 35 40 45
176 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
177 50 55 60
180 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
181 65 70 75 80
184 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
185 85 90 95
188 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
189 100 105 110
192 Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His
193 115 120 125
196 Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His
197 130 135 140
200 Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala
201 145 150 155 160
204 Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala
205 165 170 175
208 Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu
209 180 185 190
212 Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
213 195 200 205
216 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn
217 210 215 220
220 Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile
221 225 230 235 240
224 Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr
225 245 250 255
232 His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg Val
233 260 265 270
236 Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu Met
237 275 280 285
240 His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser Lys
241 290 295 300
244 Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr
245 305 310 315 320
248 Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
249 325 330 335
252 <210> SEQ ID NO: 9

RAW SEQUENCE LISTING DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387** TIME: 12:33:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

253 <211> LENGTH: 338
254 <212> TYPE: DNA
255 <213> ORGANISM: Cauliflower mosaic virus
257 <400> SEQUENCE: 9
258 ttttcacaaa gggtaatatc gggaaacctc ctcggattcc attgcccagc tatctgtcac 60
260 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120
262 ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180
264 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240
266 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
268 tcctctatat aaggaagttc atttcatttg gagaggac 338
271 <210> SEQ ID NO: 10
272 <211> LENGTH: 66
273 <212> TYPE: DNA
274 <213> ORGANISM: Artificial sequence
276 <220> FEATURE:
277 <223> OTHER INFORMATION: Nucleic acid sequence encoding the ER signal peptide
279 <400> SEQUENCE: 10
280 atgaagacta atctttttct ctttctcatc ttttcacttc tcctatcatt atcctcggcc 60
282 gaattc 66
285 <210> SEQ ID NO: 11
286 <211> LENGTH: 21
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Nucleic acid sequence encoding the vacuolar targeting sequence
293 <400> SEQUENCE: 11
294 gatcttttag tcgatactat g 21
297 <210> SEQ ID NO: 12
298 <211> LENGTH: 167
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial sequence
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Nucleic acid sequence of the Agrobacterium tumefaciens terminator
306 <220> FEATURE:
307 <221> NAME/KEY: misc_feature
308 <222> LOCATION: (162)..(162)
309 <223> OTHER INFORMATION: n is a, c, g, or t
311 <400> SEQUENCE: 12
312 taatttcatg atctgttttg ttgtattccc ttgcaatgca gggcctaggg ctatgaataa 60
314 agttaatgtg tgaatgtgtg aatgtgtgat tgtgacctga agggatcacg actataatcg 120
W--> 316 tttataataa acaaagactt tgtcccaaaa acccccccc cngcaga 167
319 <210> SEQ ID NO: 13
320 <211> LENGTH: 2186
321 <212> TYPE: DNA
322 <213> ORGANISM: Artificial sequence
324 <220> FEATURE:
325 <223> OTHER INFORMATION: nucleic acid sequence encoding high mannose human
326 glucocerebrosidase (GCD)
329 <220> FEATURE:

RAW SEQUENCE LISTING DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387** TIME: 12:33:35

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

330 <221> NAME/KEY: misc_feature
331 <222> LOCATION: (2181)..(2181)
332 <223> OTHER INFORMATION: n is a, c, g, or t
334 <400> SEQUENCE: 13
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337 ttcatcgaaa ggacagtaga aaaggaaggt ggctcctaca aatgccatca ttgcgataaa 120
339 ggaaaggcta tcgttcaaga tgcctctacc gacagtggtc ccaaagatgg acccccaccc 180
341 acgaggaaca tcgtggaaaa agaagacgtt ccaaccacgt cttcaaagca agtggattga 240
343 tgtgatatct ccactgacgt aagggatgac gcacaatccc actatccttc gcaagaccct 300
345 tcctctatat aaggaagttc atttcatttg gagaggacag gcttcttgag atccttcaac 360
347 aattaccaac aacaacaaac aacaaacaac attacaatta ctatttacaa ttacagtcga 420
349 gggatccaag gagatataac aatgaagact aatctttttc tctttctcat cttttcactt 480
351 ctcctatcat tatcctcggc cgaattcgcc cgcccctgca tccctaaaag cttcggctac 540
353 agctcggtgg tgtgtgtctg caatgccaca tactgtgact cctttgaccc cccgaccttt 600
355 cctgcccttg gtaccttcag ccgctatgag agtacacgca gtgggcgacg gatggagctg 660
357 agtatggggc ccatccaggc taatcacacg ggcacaggcc tgctactgac cctgcagcca 720
359 gaacagaagt tccagaaagt gaagggattt ggaggggcca tgacagatgc tgctgctctc 780
361 aacatccttg ccctgtcacc ccctgcccaa aatttgctac ttaaatcgta cttctctgaa 840
363 gaaggaatcg gatataacat catccgggta cccatggcca gctgtgactt ctccatccgc 900
365 acctacacct atgcagacac ccctgatgat ttccagttgc acaacttcag cctcccagag 960
367 gaagatacca agctcaagat acccctgatt caccgagccc tgcagttggc ccagcgtccc 1020
369 gtttcactcc ttgccagccc ctggacatca cccacttggc tcaagaccaa tggagcggtg 1080
371 aatgggaagg ggtcactcaa gggacagccc ggagacatct accaccagac ctgggccaga 1140
373 tactttgtga agttcctgga tgcctatgct gagcacaagt tacagttctg ggcagtgaca 1200
380 gctgaaaatg agccttctgc tgggctgttg agtggatacc ccttccagtg cctgggcttc 1260
382 acccctgaac atcagcgaga cttcattgcc cgtgacctag gtcctaccct cgccaacagt 1320
384 actcaccaca atgtccgcct actcatgctg gatgaccaac gcttgctgct gccccactgg 1380
386 gcaaaggtgg tactgacaga cccagaagca gctaaatatg ttcatggcat tgctgtacat 1440
388 tggtacctgg actttctggc tccagccaaa gccaccctag gggagacaca ccgcctgttc 1500
390 cccaacacca tgctctttgc ctcagaggcc tgtgtgggct ccaagttctg ggagcagagt 1560
392 gtgcggctag gctcctggga tcgagggatg cagtacagcc acagcatcat cacgaacctc 1620
394 ctgtaccatg tggtcggctg gaccgactgg aaccttgccc tgaaccccga aggaggaccc 1680
396 aattgggtgc gtaactttgt cgacagtccc atcattgtag acatcaccaa ggacacgttt 1740
398 tacaaacagc ccatgttcta ccaccttggc cacttcagca agttcattcc tgagggctcc 1800
400 cagagagtgg ggctggttgc cagtcagaag aacgacctgg acgcagtggc actgatgcat 1860
402 cccgatggct ctgctgttgt ggtcgtgcta aaccgctcct ctaaggatgt gcctcttacc 1920
404 atcaaggatc ctgctgtggg cttcctggag acaatctcac ctggctactc cattcacacc 1980
406 tacctgtggc atcgccaaga tcttttagtc gatactatgt aatttcatga tctgttttgt 2040
408 tgtattccct tgcaatgcag ggcctagggc tatgaataaa gttaatgtgt gaatgtgtga 2100
410 atgtgtgatt gtgacctgaa gggatcacga ctataatcgt ttataataaa caaagacttt 2160
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415 <210> SEQ ID NO: 14
416 <211> LENGTH: 526
417 <212> TYPE: PRT
418 <213> ORGANISM: Artificial sequence
420 <220> FEATURE:
421 <223> OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
423 <400> SEQUENCE: 14
425 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387** TIME: 12:33:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 162
Seq#:13; N Pos. 2181

VERIFICATION SUMMARY DATE: 11/03/2005
PATENT APPLICATION: **US/10/554,387** TIME: 12:33:36

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\11032005\J554387.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:120
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:2160

Raw Sequence Listing before editing (for reference only)

PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/554,387

DATE: 11/01/2005
TIME: 11:00:57

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11012005\J554387.raw

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     3 <110> APPLICANT: Shaaltiel, Yoseph
     4       Baum, Gideon
     5       Sharon Hashmueli
     6       Ayala Lewkowicz
     7       Bartfeld, Daniel
     9 <120> TITLE OF INVENTION: PRODUCTION OF HIGH MANNOSE PROTEINS IN PLANT CULTURE
    11 <130> FILE REFERENCE: 30570
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/554,387
C--> 13 <141> CURRENT FILING DATE: 2005-10-25
    13 <160> NUMBER OF SEQ ID NOS: 14
    15 <170> SOFTWARE: PatentIn version 3.3
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ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

P.2

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   162 <210> SEQ ID NO: 8
   163 <211> LENGTH: 335
   164 <212> TYPE: PRT
   165 <213> ORGANISM: Homo sapiens
   167 <400> SEQUENCE: 8
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   170 1               5                  10                  15
   173 Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro
   174             20                  25                  30
   177 Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg
   178         35                  40                  45
   181 Met Glu Leu Ser Met Gly Pro Ile Gln Ala Asn His Thr Gly Thr Gly
   182     50                  55                  60
   185 Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys Phe Gln Lys Val Lys Gly
   186 65                  70                  75                  80
   189 Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu Asn Ile Leu Ala Leu
   190                 85                  90                  95
   193 Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser Glu Glu
   194             100                 105                 110
   197 Gly Val Arg Leu Leu Met Leu Asn Asp Gln Arg Leu Leu Leu Pro His
   198         115                 120                 125
   201 Trp Ala Lys Val Val Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His
   202     130                 135                 140
   205 Gly Ile Ala Val His Trp Tyr Leu Asp Phe Leu Ala Pro Ala Lys Ala
   206 145                 150                 155                 160
   209 Thr Leu Gly Glu Thr His Arg Leu Phe Pro Asn Thr Met Leu Phe Ala
   210                 165                 170                 175
   213 Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser Val Arg Leu
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RAW SEQUENCE LISTING DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387 TIME: 11:00:57

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11012005\J554387.raw

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     214                 180                 185                 190
     217 Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
     218         195                 200                 205
     221 Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn
     222     210                 215                 220
     225 Pro Glu Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile
     226 225                 230                 235                 240
     229 Ile Val Asp Ile Thr Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr
E--> 235             ~~245~~ 245         ~~250~~ 250         ~~255~~ 255
     237 His Leu Gly His Phe Ser Lys Phe Ile Pro Glu Gly Ser Gln Arg Val
E--> 238             260                 265                 270
     241 Gly Leu Val Ala Ser Gln Lys Asn Asp Leu Asp Ala Val Ala Leu Met
E--> 242         275                 280                 285
     245 His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn Arg Ser Ser Lys
E--> 246     290                 295                 300
     249 Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu Thr
E--> 250 305                 310                 315                 320
     253 Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln
E--> 254                 325                 330                 335
     426 <210> SEQ ID NO: 14
     427 <211> LENGTH: 526
     428 <212> TYPE: PRT
     429 <213> ORGANISM: Artificial sequence
     431 <220> FEATURE:
     432 <223> OTHER INFORMATION: High mannose human glucocerebrosidase (GCD)
     434 <400> SEQUENCE: 14
     436 Met Lys Thr Asn Leu Phe Leu Phe Leu Ile Phe Ser Leu Leu Leu Ser
     437 1               5                   10                  15
     440 Leu Ser Ser Ala Glu Phe Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly
     441             20                  25                  30
     444 Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser Phe
     445         35                  40                  45
     448 Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu Ser
     449     50                  55                  60
     452 Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln Ala
     453 65                  70                  75                  80
     456 Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln Lys
     457                 85                  90                  95
     460 Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala
     461             100                 105                 110
     469 Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys
     470         115                 120                 125
     473 Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro
     474     130                 135                 140
     477 Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp Thr
     478 145                 150                 155                 160
     481 Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp Thr
     482                 165                 170                 175
     485 Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln Arg
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RAW SEQUENCE LISTING DATE: 11/01/2005
PATENT APPLICATION: US/10/554,387 TIME: 11:00:57

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\11012005\J554387.raw

```
486                 180                 185                 190
489 Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
490         195                 200                 205
493 Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly
494     210                 215                 220
497 Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp
498 225                 230                 235                 240
501 Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn
502                 245                 250                 255
505 Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly
506             260                 265                 270
509 Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly Pro
510         275                 280                 285
513 Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu Asp
514     290                 295                 300
517 Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr Asp
518 305                 310                 315                 320
521 Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
522                 325                 330                 335
525 Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu
526             340                 345                 350
529 Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys
530         355                 360                 365
533 Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln
534     370                 375                 380
537 Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly Trp
538 385                 390                 395                 400
541 Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp Val
542                 405                 410                 415
548 Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp Thr
549             420                 425                 430
552 Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys Phe
553         435                 440                 445
556 Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn
557     450                 455                 460
560 Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val
561 465                 470                 475                 480
564 Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp
565                 485                 490                 495
568 Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile His
569             500                 505                 510
572 Thr Tyr Leu Trp His Arg Gln Asp Leu Leu Val Asp Thr Met
573         515                 520                 525
```

E--> 580 12
E--> 582 2
E--> 585 pcdo
E--> 588 12022/ph/00

VERIFICATION SUMMARY DATE: 11/01/2005
PATENT APPLICATION: **US/10/554,387** TIME: 11:00:58

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\11012005\J554387.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:242 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:246 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:250 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:254 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
L:327 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:120
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:2160
L:580 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:582 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:14
L:585 M:333 E: Wrong sequence grouping, Amino acids not in groups!
L:585 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1
L:588 M:252 E: No. of Seq. differs, <211> LENGTH:Input:526 Found:527 SEQ:14